REMARKS

Status of the Claims.

Claims 45-86 are pending with entry of this amendment, claim 1 being cancelled and claims 45-86 being added herein. Support for claims 45-86 is found generally throughout the specification. Specific support for the recited chromosomal regions is found, for example, at pages 10, 26, 35, 72, 73, 74, 75, 81, 89, 91, 93, 94, 95, 96, 97, 108, 109. Therefore, these amendments introduce no new matter.

35 U.S.C. § 102.

Claim 1 was rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Montgomery *et al.* (*Proc. Natl. Acad. Sci. USA* (1983) 80:5724-5728. Office Action, page 2. This rejection is moot in light of the cancellation of claim 1.

Obviousness-Type Double-Patenting.

Claim 1 was rejected under the judicially created doctrine of obviousness-type double patenting as unpatentable over: claims 1-53 of U.S. Patent No. 6,335,167; claims 1-19 of U.S. Patent No. 6,159,685; claims 1-42 of U.S. Patent No. 5,976,790; claims 1-12 of U.S. Patent No. 5,965,362; claims 1-24 of U.S. Patent No. 5,856,057; claims 1-27 of U.S. Patent No. 5,721,098; claims 1-54 of U.S. Patent No. 5,665,549. The cancellation of claim 1 also renders this rejection moot.

Conclusion

The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If a telephone conference would expedite prosecution of this application, the Examiner is invited to telephone the undersigned at (510) 769-3509.

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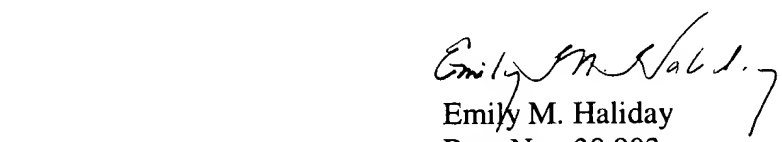
Respectfully submitted,



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APPENDIX A

"MARKED UP" CLAIMS ILLUSTRATING THE AMENDMENTS MADE TO THE CLAIMS OF 09/912,818 WITH ENTRY OF THIS AMENDMENT

1. (Canceled)

--45. (Amended) A method of detecting an amplification or gain of unique sequences at at least one chromosomal region selected from the group consisting of:

on human chromosome 1,
about position p22 to the centromere;
the q arm;
the centromere to about position p32;
about position q31 to qter;
about position q32;
about position q32 to qter;
on human chromosome 2,
the p arm;
on human chromosome 3,
about position p14;
about position p14 to qter;
about position p22 to pter;
about position q26 to qter;
on human chromosome 4,
the p arm;
about position q32 to about position q34;
on human chromosome 5,
the p arm;
about position q31 to qter;
about position q32 to qter;
on human chromosome 6,

the p arm;

the centromere to about position p21;

about position p23 to pter;

the centromere to about position q21;

about position q12 to about position q13;

about position q21;

about position q21 to about position q22;

on human chromosome 7,

the p arm;

the centromere to about position p12;

about position p21;

pter to about position q31;

the q arm;

about position q22 to about position q32;

on human chromosome 8,

about position p12;

the q arm;

about position q21;

about position q21 to about position q23;

about position q21 to qter;

about position q22 to about position q23;

about position q22 to qter;

about position q23 to about position q24;

about position q23 to qter;

about position q24;

on human chromosome 10,

the p arm;

the centromere to about position q21;

about position q22;

on chromosome 11,

about position p15;

the q arm;

about position q13;

on human chromosome 12,

the p arm;

the q arm;

about position q14 to about position q15;

about position q21;

about position q21 to about position q23;

about position q24;

on human chromosome 13,

about position 22 to qter;

about position q31 to qter;

on human chromosome 14,

the q arm;

about position q24 to qter;

about position q31;

about position q31 to qter;

on human chromosome 15,

about position q21 to qter;

about position q24;

about position q25;

about position q26;

entire human chromosome 16;

on human chromosome 16,

the p arm;

the q arm;

about position q23 to about position q24;

on human chromosome 17,

the centromere to about position q24;

about position q12;

about position q21 to qter;

about position q22 to about position q23;

about position q22 to about position q24;

about position q22 to qter;

about position q24 to qter;

on human chromosome 18,

the p arm;

on human chromosome 19,

the q arm;

about position q13;

about position q13 to qter;

entire human chromosome 20;

on human chromosome 20,

the p arm;

the q arm;

about position q12 to about position q13;

about position q13;

about position q13 to qter;

about position q34;

qter;

entire chromosome 21;

entire chromosome 22;

on the human X chromosome,

the p arm,

in a test sample, said method comprising:

(a) labelling nucleic acids from the test sample and from a control sample with different labels;

(b) contacting said labelled nucleic acids from each sample with a plurality of target nucleic acids, wherein either the labelled nucleic acids or the target nucleic acids, or both, have had repetitive sequences, if initially present, blocked and/or removed; and

(c) comparing the intensities of the signals from labelled nucleic acids hybridized to each

target nucleic acid, thereby allowing detection of the presence or absence of the amplification or gain in the test sample.

46. The method of claim 45, wherein the step of comparing the intensities of the signals from the labelled nucleic acids comprises determining the ratio of the intensities of the signals as a function of position in the target nucleic acids.

47. The method of claim 45, wherein the amplification is of the q arm of human chromosome 1.

48. The method of claim 45, wherein the amplification is of the p arm of human chromosome 7.

49. The method of claim 45, wherein the amplification is of the q arm of human chromosome 8.

50. The method of claim 45, wherein the amplification is at about position q24 on human chromosome 8.

51. The method of claim 45, wherein the amplification is of the q arm of human chromosome 11.

52. The method of claim 45, wherein the amplification is at about position q13 on human chromosome 11.

53. The method of claim 45, wherein the amplification is of the q arm of human chromosome 12.

54. The method of claim 45, wherein the amplification is of the q arm of human chromosome 14.

55. The method of claim 45, wherein the amplification is of the q arm of human chromosome 16.

56. The method of claim 45, wherein the amplification is at about position q22 to about position q24 on human chromosome 17.

57. The method of claim 45, wherein the amplification is of the q arm of human chromosome 20.

58. The method of claim 45, wherein the target nucleic acids comprise at least one metaphase chromosome.

59. The method of claim 45, wherein said nucleic acid sample comprises genomic DNA molecules.

60. The method of claim 45, wherein said nucleic acid sample comprises DNA amplified from said test sample.

61. The method of claim 45, wherein said nucleic acid sample comprises complementary DNA.

62. (Amended) A method of detecting a deletion of unique sequences at at least one chromosomal region selected from the group consisting of:

on human chromosome 9, the p arm;
on human chromosome 16,
the q arm;
about position q22;
on human chromosome 17, the p arm;
in a test sample, said method comprising:

(a) labelling nucleic acids from the test sample and from a control sample with different labels;

(b) contacting said labelled nucleic acids from each sample with a plurality of target nucleic acids, wherein either the labelled nucleic acids or the target nucleic acids, or both, have had repetitive sequences, if initially present, blocked and/or removed; and

(c) comparing the intensities of the signals from labelled nucleic acids hybridized to each target nucleic acid, thereby allowing detection of the presence or absence of the deletion in the test sample.

63. The method of claim 62, wherein the step of comparing the intensities of the signals from the labelled nucleic acids comprises determining the ratio of the intensities of the signals as a function of position in the target nucleic acids.

64. The method of claim 62, wherein the target nucleic acids comprise at least one metaphase chromosome.

65. The method of claim 62, wherein said nucleic acid sample comprises genomic DNA molecules.

66. The method of claim 62, wherein said nucleic acid sample comprises DNA amplified from said test sample.

67. The method of claim 62, wherein said nucleic acid sample comprises complementary DNA.

68. A method for detecting a copy number variation in a suspected breast cancer sample by detecting an amplification or gain of unique sequences at at least one chromosomal region selected from the group consisting of:

on chromosome 17, about position q22 to about position q24;
on chromosome 20,
the q arm;
about position q13,
said method comprising:

(a) contacting a probe that binds selectively to a target polynucleotide sequence of said region with a nucleic acid sample prepared, directly or indirectly, from said suspected breast cancer sample, wherein said nucleic acid sample comprises said target polynucleotide sequence and said probe is contacted with said sample under conditions in which said probe forms a stable hybridization complex with said target nucleic acid sequence; and

(b) detecting said hybridization complex.

69. The method of claim 68, wherein said probe is labeled.

70. The method of claim 68, wherein said nucleic acid sample is labeled.

71. The method of claim 68, wherein the amplification is at about position q22 to about position q24 on human chromosome 17.

72. The method of claim 68, wherein the amplification is of the q arm of human chromosome 20.

73. The method of claim 68, wherein the amplification is at about position q13 on human chromosome 20.

74. The method of claim 68, wherein said nucleic acid sample comprises genomic DNA molecules.

75. The method of claim 68, wherein said nucleic acid sample comprises DNA amplified from said suspected breast cancer sample.

76. The method of claim 68, wherein said nucleic acid sample comprises complementary DNA.

77. A method for detecting a copy number variation by detecting an amplification or gain of unique sequences at at least one chromosomal region selected from the group consisting of:

on human chromosome 1,
the centromere to about position p32;
about position q31 to qter;
about position q32;
about position q32 to qter;
on human chromosome 2,
the p arm;
on human chromosome 3,
about position p14;
about position p14 to qter;
about position p22 to pter;

about position q26 to qter;

on human chromosome 4,

the p arm;

about position q32 to about position q34;

on human chromosome 5,

the p arm;

about position q31 to qter;

about position q32 to qter;

on human chromosome 6,

the p arm;

the centromere to about position p21;

about position p23 to pter;

the centromere to about position q21;

about position q12 to about position q13;

about position q21;

about position q21 to about position q22;

on human chromosome 7,

the p arm;

the centromere to about position p12;

about position p21;

pter to about position q31;

the q arm;

about position q22 to about position q32;

on human chromosome 8,

about position q21;

about position q21 to about position q23;

about position q21 to qter;

about position q22 to about position q23;

about position q22 to qter;

about position q23 to qter;

on human chromosome 10,

the p arm;

the centromere to about position q21;

about position q22;

on chromosome 11,

about position p15;

the q arm;

on human chromosome 12,

the p arm;

the q arm;

about position q14 to about position q15;

about position q21;

about position q21 to about position q23;

about position q24;

on human chromosome 13,

about position 22 to qter;

about position q31 to qter;

on human chromosome 14,

the q arm;

about position q24 to qter;

about position q31;

about position q31 to qter;

on human chromosome 15,

about position q21 to qter;

about position q24;

about position q26;

entire human chromosome 16;

on human chromosome 16,

the p arm;

the q arm;

about position q23 to about position q24;

on human chromosome 17,

the centromere to about position q24;

about position q21 to qter;

about position q22 to about position q23;

about position q22 to qter;

about position q24 to qter;

on human chromosome 18,

the p arm;

on human chromosome 19,

the q arm;

about position q13;

about position q13 to qter;

entire human chromosome 20;

on human chromosome 20,

the p arm;

about position q12 to about position q13;

about position q13 to qter;

about position q34;

qter;

entire chromosome 21;

entire chromosome 22;

on the human X chromosome,

the p arm,

in a test sample, said method comprising:

(a) contacting a probe that binds selectively to a target polynucleotide sequence of said region with a nucleic acid sample prepared, directly or indirectly, from said suspected breast cancer sample, wherein said nucleic acid sample comprises said target polynucleotide sequence and said probe is contacted with said sample under conditions in which said probe forms a stable hybridization complex with said target nucleic acid sequence; and

(b) detecting said hybridization complex.

78. The method of claim 77, wherein said probe is labeled.

79. The method of claim 77, wherein said nucleic acid sample is labeled.

80. The method of claim 77, wherein the amplification is of the q arm of human chromosome 7.

81. The method of claim 77, wherein the amplification is of the q arm of human chromosome 12.

82. The method of claim 77, wherein the amplification is of the q arm of human chromosome 14.

83. The method of claim 77, wherein the amplification is of the q arm of human chromosome 16.

84. The method of claim 77, wherein said nucleic acid sample comprises genomic DNA molecules.

85. The method of claim 77, wherein said nucleic acid sample comprises DNA amplified from said suspected bladder cancer sample.

86. The method of claim 77, wherein said nucleic acid sample comprises complementary DNA.--

APPENDIX B

"MARKED UP" PARAGRAPHS ILLUSTRATING THE AMENDMENTS MADE TO THE SPECIFICATION OF 09/912,818 WITH ENTRY OF THIS AMENDMENT

1. The following paragraph is substituted for the paragraph beginning at page 1, line 6:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of Application No. 09/311,835, filed May 14, 1999, which is a continuation of Application No. 08/565,304, filed November 27, 1995, which is a divisional of Application No. 08/223,905, filed April 6, 1994 (now abandoned), which is a continuation of Application No. 08/132,172, filed October 6, 1993 (now abandoned), which is a continuation-in-part of Application No. [07/696,948] 07/969,948, filed October 20, 1992 (now abandoned), which is a continuation-in part of Application No. 07/846,659, filed March 4, 1992 (now abandoned).